

161



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# Consensus

re3 (15-45)  
hcj7.pep (15-45)  
ny1.pep (15-45)  
GE11.2 (15-45)  
s71957.p (15-45)  
ec10 (15-45)  
sp2.tc (15-45)  
M2.2 (15-45)  
rela (15-45)  
168 (15-45)  
M1.5 (15-45)  
hpcprcla.p1 (14-44)  
gm2.tc (15-45)  
s71864.p1 (15-45)  
i15.tc (15-45)  
sp1.tc (15-45)  
re37b (15-45)  
re39 (15-45)  
hpchcj2.p (15-45)  
hpccgenom.p1 (15-45)  
hpcprc4a.p2 (14-44)  
hpcprc11a.p1 (4-34)  
re72b (15-45)  
hpcprc3a.p1 (4-34)  
re70 (15-45)  
re42 (15-45)  
63 (15-45)  
hcvj (15-45)  
hcvj1 (15-45)  
re38 (15-45)  
bk (15-45)  
re5 (15-45)  
re35 (15-45)  
re36 (15-45)  
re54 (15-45)  
re56 (15-45)  
64 (15-45)  
re62 (15-45)  
re41 (15-45)  
hpcvjk3.p (15-45)  
jk2 (15-45)  
hcv1 (15-45)  
us5.tc (15-45)

.T.VTGG.AARTT.G..SLF..G.SQ.IQLI 31  
A.YA..AAQGH.ANSFV...RS.A..NLK.V 45  
S.Q....Q..H.VR.VA.I.SP.SR.D.S.. 45  
S.R....QQG.AVH.IA...SL.A..K...V 45  
S.H.M.AQQG.VAK.FT...GP.PA.K.... 45  
S.H...AVQGH.SIR.LT...TS.PA.K...V 45  
E.H....I..K..ASLTG..NL.AK.N.... 45  
E.H....N.G.AAA.IAG..TL.AK.NV... 45  
Q.R....T..QS.ARIAG..SL.AR.N.... 45  
Q.H.M..T.G.NAY.LT.FLSV.A..K.... 45  
E.H.M..A.SS..YRFA...TS.PA.K...V 45  
E.H....S..S..ATFSK..MP.A..N.... 45  
G.TRV..A.....SSFA..LTH.P..N...V 44  
G.H....A...DAFRFS...TR.P..N.... 45  
A.NM...AP....YKLT..SY.A..K.... 45  
HNH....TS..N.F.ITT..TQ.P..KL..V 45  
G.H....A...NAHSLT..LAP.A..K.... 45  
T.R.S..T..H..A.LT...SP.PR.N.H.V 45  
T.H.S..T.G...ASLT.F.AP.A..R...V 45  
T.H....ATGH..S.IA...LP.A..K.... 45  
D.YAS..AQG.S.L.FT...TP.A..K.... 45  
D.YAS..A.G.A.Y.IT...AP.A..N.... 44  
R.YAS..A.G...H.FT...ST.AR.N.... 34  
Q.Y...K..Q.VS.FTG..SS.P..K.... 45  
D.Y.S..A...SIS.FT...TP.A..K...V 34  
S.Y....E.S...R.FA...TL.S..K.... 45  
N.Y....S.G.AVA.FAG.LQP.AK.NV... 45  
H.R....QV.FR.H.LV...TQ.P..K...V 45  
H.H....RV.SS.QSLV.WLSQ.P..K...V 45  
H.R....VQGHV.STLT...RP.A..K...V 45  
N.R....VQG.D.S.LV...SL.P..K...V 45  
D.H....AQ.K..NRLV.M.AS.P..K.... 45  
E.H....AS....QRFT.F.DL.P..K...V 45  
T.YM...AN....Q.FV...TP.PA.K...V 45  
E.H....TS....Q.FV...SA.A..K...V 45  
G.H....Q....QSFT...SP.PQ.K.... 45  
R.H....K..H..K.FA...TP.P..N.... 45  
E.R...AVQGHGAL.LA...TP.P..K.... 45  
E.R...AI.G..ASSFAG..TS.A..K...V 45  
E.R...QQVG...QSLT...TP.P..T.... 45  
Q.R...AQVG...SSLT...TP.P..N...V 45  
R.Q...AQ.GH..S.LA...TP.P..K...V 45  
E.H....S.GH.VS.FV..LAP.AK.NV... 45  
E.H....S.GH.VT.IA...TS.AK.N.... 45

FIG. 2A



S.H....T.H.VA.FS...TV.PK.N....  
E.H....A.Y.AA.LA...TS.AK.N....  
E.H....S.G...A.LVG.LTP.AK.N....  
G.H....S.G.A.A.IAG.LTP.AR.N...V  
K.H....S....S.IA...LTP.AK.NV...  
K.Y....SQ.QA.F.FT...LQQ.AK.N....  
E.T....S.HGAL.IA...NQ.AR.N....  
E.Y....AS.S.FTLVG..KQ.SQ.N...V  
Q.Y.S.SSG...S.LV.I.SP.A.NL...  
E.Y.S.A.Q..ARFAGF.QS.AK.N....  
E.Y.S.S..Q..A.FVR..ET.PK.N....  
S.Y.S.AQ..AAQ.IT...SR.S.K...V  
S.Y...TQG.AAS.LT...SA.A.N....  
N.Y.S.T.GH.GH.LTA..SP.A.N....  
S.I.S.TV...HSLA...TQ.A.K....  
E.YTS.A.SH..STLA..SP.A.R...V  
H.LT..H...L.S.FAG..TP.P.R....  
E.I.S.Q...AMS.LV...TP.AK.N....  
E.YTS..N.GH.MT.IVRF.AP.PK.NVH..  
T.YT...N.....QALT.F.SP.AK.D....  
E.YT...ST...Q.LV...SR.AK.D....  
A.YTS..S.....Q.FA...SL.SQ.K...V  
A.YT...SV...H.FS...SQ.AK.N....  
V.YT...SQ..H.QSVT.F.TQ.PA.R....  
H.YT...TV..S.Q.LVGFLSP.P.N....  
T.Y.SV.H.SQ..RRVA.F.SP.SA.K...V  
T.T.S..H.SQI.R.VT.F.SP.SA.K...V  
K.SL..VTR..AAARLTA..SS.P.R....  
G.SL..AR..AAS.LAG..SS.P.R....  
V.Q.SPPQ.GY..SVLTGILSP.AK.N...V  
V.Q.S..Q.GY..SVLTGILSP.AK.N...V  
G.YTV..AS.F..SRLT...AL.P.R...V  
N.HTV..TEGFA.QRLT...AL.P.K....  
S.RTA..AQ.FN.Y.VA.I.SP.P.R...V  
Q.HTV..ST.HNARTLTGM.SL.AR.K....  
N.RTV.A.S..A..R.FT.M.SS.SK.NL...  
Q.RTV..QVGHSVR.FT...SA.SA.N....  
E.HT..AVSGH..NVLT...SS.S.N....  
V.RT..EV...ANTFA...TT.P.N...I  
T.YSS.QE.G..VA.FAG..TT.AK.NLY..  
S.S.V..RQ.SA.FRFT.F.SR.PT.E.K..  
N.YT.A.SM.QSIYRLTDI.ST.P.KL...V  
R.ILMA.RQ.EV.QSFPG..SLAP..K.H..  
D.YA...SV.SIMA.IARF.SP.AR.D....  
E.YA..AS.GHDVSSFAR..AP.AR.N...-  
E.HR...S...S.A.VA...TP.AR.N....  
N.RAV.MVQS...YALT...DS.AA.KL..V

[illegible]

FIG. 2B



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Hutchinson	Strains:	395	407	
H77	384	ETHVTGGSAGRTTAGLVGLLTPGAKQNIQLI <sup>41</sup>		1977
H90		-----SVL-IASF--R-P-----		1990
HC-J4	Strains:	395	407	
HPCJ483	384	ETYTSGGAASHTTSTLASLSPGASQRIQLV <sup>414</sup>		1983
J48711		A-----V-----RFT-----S-----		
J48712		A-----AV-----RFT-F--S-----		
J48713		A-----AV-----RFT-----S-----		1987
J48714		A-----AV-----GFT-----S-----		
J48715		-----RV-G-----GFT-----S-----		
HPCJ491		A-----V-GR-----GFT-----S-----K-----		
J49120		--H-T-RV-G-----RFT-----S-----K-----		
J49121		--H-T-RVVG-----GFT-----S-----K-----		1991
J49122		--H-T-RV-GR-----GFT-----S-----K-----		
J49126		T-----V-GR-----GFT-----S-----K-----		
J49127		K-----RFT-----S-----K-----		
NY	Strains:	395	407	
NY1.1	384	STRVTGGQQGRAVHGIA SLFSLGASQKIQLV <sup>414</sup>		t <sub>0</sub>
NY1.2		-----Q-F-----R-----E-----		
NY1.3		-----N-----		
NY2.1		-----H-A-SLT---R-----N-----		6mo
NY2.2		-----H-A-SLT---R-----N-----		
NY3.1		N-----R-----A-SLT---P-----N-----		
NY3.2		N-----R-----A-SLT---P-----N-----		-8mo
NY3.3		G-----R-----A-SLT---P---EN-R---		
NY3.4		---S-----A-SLT---T-----N-----		
NY3.5		--H---AL-----AY---T-FL-H-P-----		
NY4.1		--Q-M-----AYSL---L-P---N-----		
NY4.2		--Q-M-----AYSL---LGP-----		14mo
NY4.3		--Q-M-----AYSL---L-P-----		
RS	Strains:	395	407	
RS1.1.	384	RTRTVGGQVGHSVRGFTSLFSAGSAQNIQLI <sup>414</sup>		t <sub>0</sub>
RS1.2.		Q-----		
RS1.3.		Q-----D-----		
RS2.4.		Q-----L-----		2mo
RS3.1.		Q-----L-----		6mo
RS4.1.		Q-----M-G---L-----R-----		
RS4.2.		Q-H---M-G---L-----		8mo
RS5.1.		Q-H---M-G---L-N-----		11mo

FIG. 3



Amino Acid Position:

**FIG. 4**

*	\$#	*	##	##	#	±	±	##	±	a	#	*	*a	##	#	##	##	a	a	\$#	##		
384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407

% Conserved AA Character for Each AA Position:

49	99	58	100	100	100	97	73	77	100	75	90	100	63	89	100	99	93	100	100	87	87	100	100
----	----	----	-----	-----	-----	----	----	----	-----	----	----	-----	----	----	-----	----	----	-----	-----	----	----	-----	-----

Legend

- #\$ 99-100% identical amino acids (invariantly conserved)
- ## 100% conserved amino acid substitutions (invariantly conserved)
- # 90-99% conserved amino acid substitutions
- a 80-89% conserved amino acid substitutions
- ± 70-79% conserved amino acid substitutions
- \* 49-69% conserved amino acid substitutions (highly variable)

\*a position with the least conserved amino acid substitutions in temporarily sequential time points in individual patients (Figure 3).

Notes:

Positions 403 (F,L), 406 (G,A) and 407 (A,P,S) utilize only 2 or 3 amino acids of homologous character, respectively.

Position 394 represents the only strongly conserved basic amino acid, all others conserved for hydrophobic character and/or size in the case of amino acid position 407.

Position 398 appears to be least conserved between AA 395-407 in sequentially temporal Hc(390)CH isolates in individual patients (see Fig. 3).

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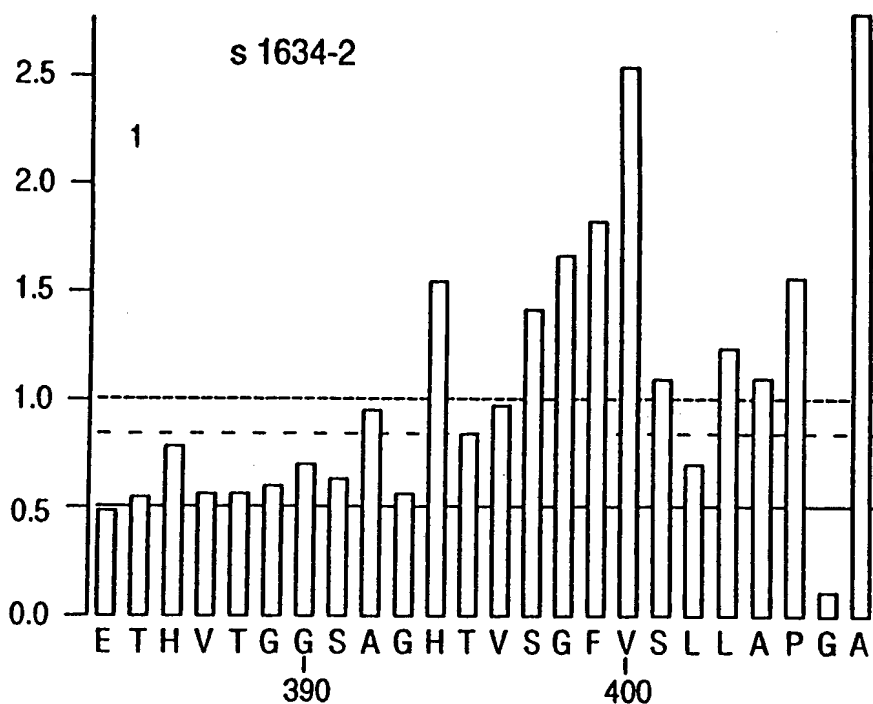


FIG.5A

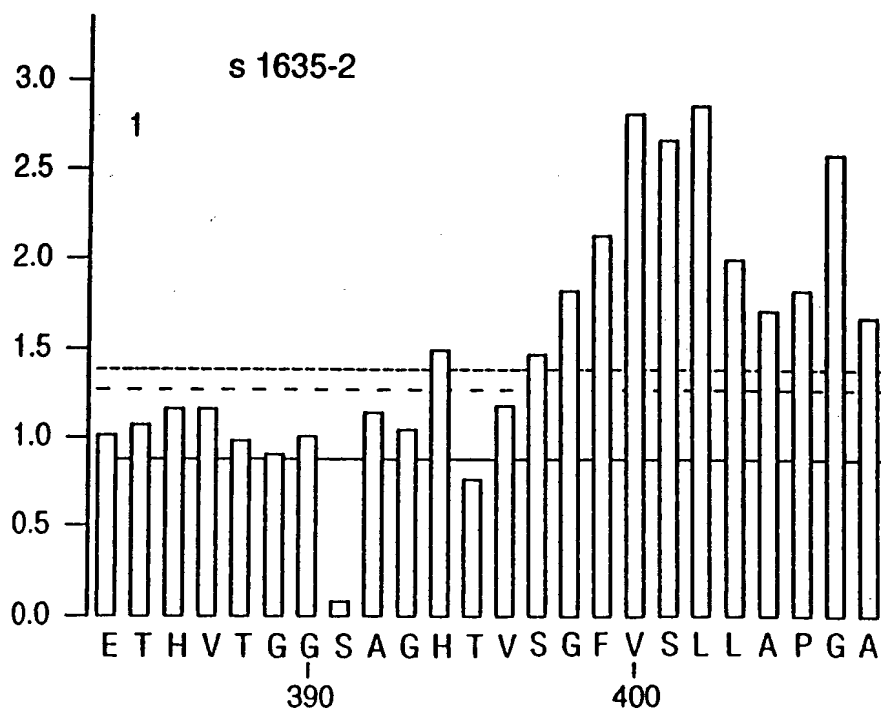


FIG.5B



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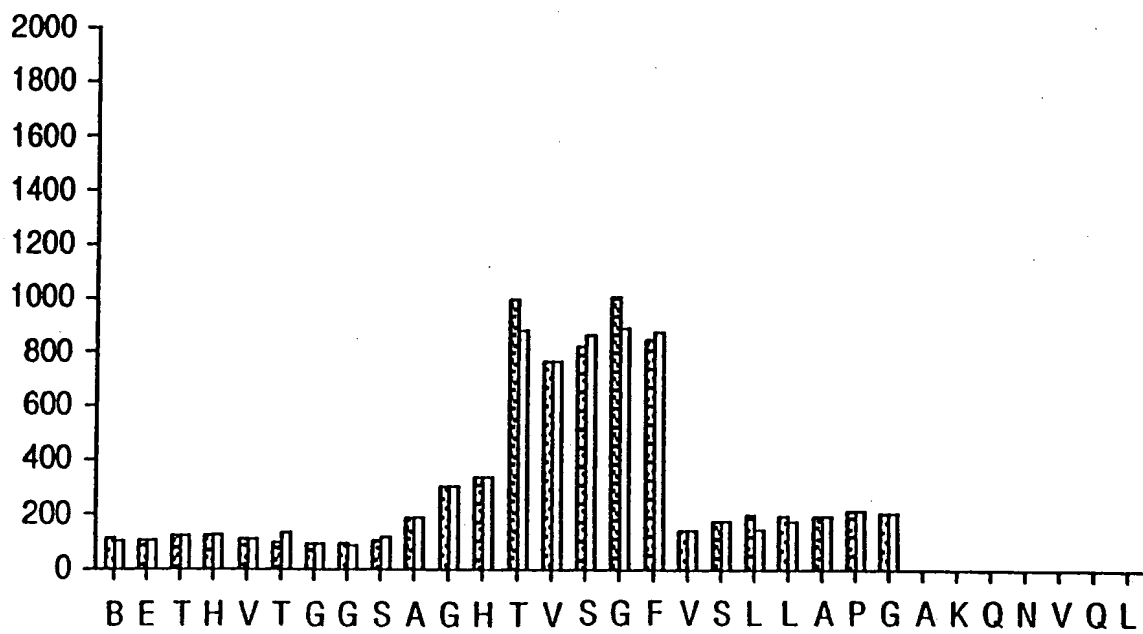


FIG.6

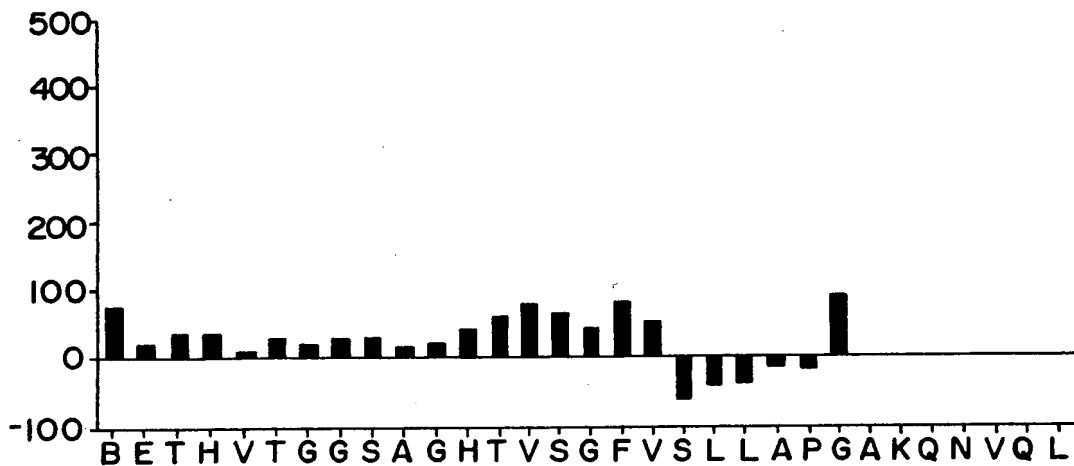


FIG.7A

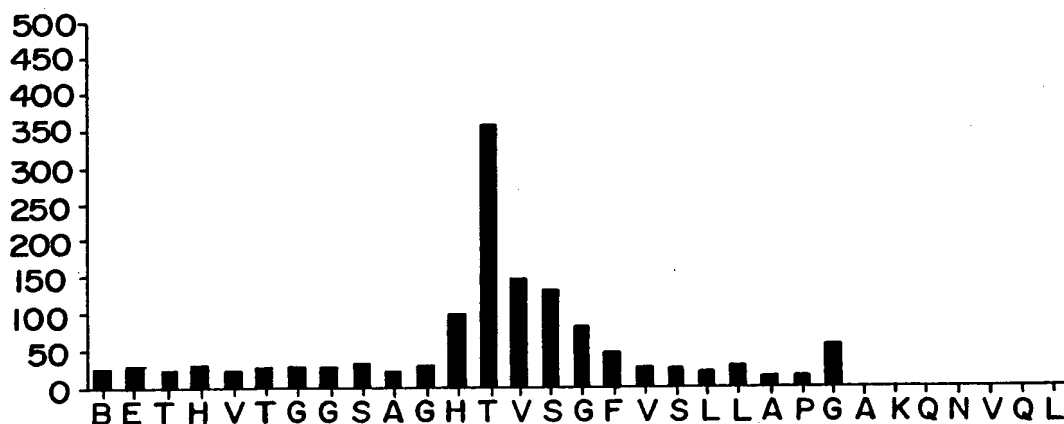


FIG.7B

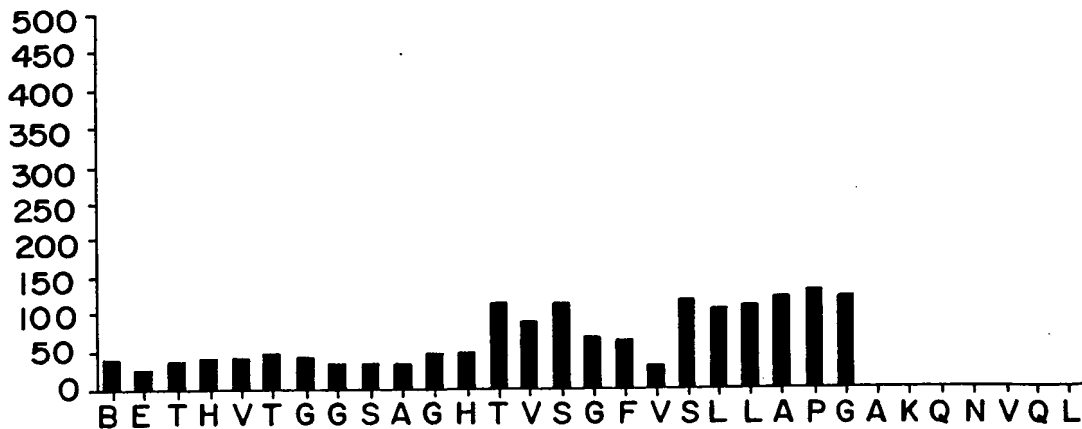


FIG.7C